

SEQUENCE LISTING

<110> King, George L.
Abrahamson, Susan
Pugsley, Michael

<120> Modulation of Pericyte Proliferation

<130> 27129/36739A

<150> 60/250,542

<151> 2000-12-01

<160> 15

<170> PatentIn version 3.1

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Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
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cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt	246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
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aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	

atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
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Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
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Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
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Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys	
170 175 180 185	
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Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser	
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Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala	
205 210 215	
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Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His	
220 225 230	
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His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala	
235 240 245	
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His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr	
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Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg	
270 275 280	
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Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe	
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Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys	
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Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln	
315 320 325	
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Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala	
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Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His	
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Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly	
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Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile	
380 385 390	
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Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val	
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ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc	1398
Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe	
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Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln	
430 435 440	
cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa	1491
Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys	
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tcttcgactc agattcagaa atgatctaaa cagcaggaaa cattattcat tggaaaagtg	1671
catggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatat	1731
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Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
35 40 45

His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
50 55 60 65

Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
70 75 80

Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
85 90 95

Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
100 105 110

Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
115 120 125

Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
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150 155 160

Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
165 170 175

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180 185 190

Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
195 200 205

Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
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Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
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Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
245 250 255

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260 265 270

Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
275 280 285

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Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
310 315 320

Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
325 330 335

Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
340 345 350

Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
355 360 365

Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
370 375 380 385

Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
390 395 400

Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
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Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
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